The 26th Hot Spring Harbor International Symposium

−Trans-Omics: New Approaches in Biology and Medicine−

Medical Institute of Bioregulation, Kyushu University

November 2-3, 2016

Collaborative Research Station Hall I, Hospital Campus, Kyushu University, Fukuoka, JAPAN

Wednesday, November 2, 2016

10:00-10:05 Opening Remarks: **Yusaku Nakabeppu** (Director of Medical Institute of Bioregulation)

Session 1: Signaling Networks Chair: **Takeshi Bamba**

10:05-10:30 S-01: **Mariko Okada** (Osaka University, Japan)

Multiple-scale cooperativity in signal-transcription network for cellular commitment

10:30-10:55 S-02: **Hiroyuki Kubota** (Kyushu University, Japan)

Trans-omic analysis of insulin action-toward in vivo trans-omic analysis-

10:55-11:30 S-03: **Uwe Sauer** (ETH Zurich, Switzerland)

Coordination of metabolism through metabolite-protein interactions

11:30-11:40 Group Photos

11:40-13:00 Lunch (Transomics meeting by invitation only)

Session 2: Transcription, Translation and Robustness Chair: **Mikita Suyama**

13:00-13:25 S-04: **Hisao Moriya** (Okayama University, Japan)

Consequences of protein overexpression

13:25-13:50 S-05: **Yasuyuki Ohkawa** (Kyushu University, Japan)

The baseline of transcription level is determined by selective incorporation of histone H3 variants

13:50-14:25 S-06: **Timothy J. Stasevich** (Colorado State University, USA)

Real-time imaging of single mRNA translation dynamics in living cells

14:25-14:45 Coffee break

Session 3: **Short Talks by Young Scientists** Chair: **Tohru Ishitani**

14:45-16:45 Short talks of 12 minutes each (see p.4 for details)

16:45-17:05 Coffee break

Session 4: **Development and Differentiation** Chair: **Atsushi Suzuki**

17:05-17:30 S-07: **Hiroyuki Sasaki** (Kyushu University, Japan)

Multiple functions of the epigenetic regulator UHRF1 in mouse oocytes revealed by trans-omics approaches

17:30-17:55 S-08: **Akira Nakamura** (Kumamoto University, Japan)

Search for new factors that direct germ cell formation in the Drosophila embryo

17:55-18:20 S-9: **Naoki Irie** (University of Tokyo, Japan)

Why are vertebrates’ organogenesis stages evolutionarily conservative?

19:00- **Dinner party** (by invitation only)

Thursday, November 3, 2016

Session 5: **Disease_I** Chair: **Hiroki Shibata**

10:30-10:55 S-10: **Tatsuhiko Tsunoda** (Tokyo Medical and Dental University, Japan)

Trans-omic analysis strategy for precision medicine

10:55-11:20 S-11: **Yoshiyuki Minegishi** (Tokushima University, Japan)

Identification of the molecular pathogenesis of hyper-IgE syndrome

11:20-11:55 S-12: **Yong Hou** (Beijing Genomics Institute, China)

Efforts to push single cell trans-omics for cancer research

11:55-13:30 Lunch

Session 6: **Disease_I I** Chair: **Yoshihiro Yamanishi**

13:30-13:55 S-13: **Keiichi Nakayama** (Kyushu University, Japan)

Next-generation proteomics unveils a global landscape of cancer metabolism

13:55-14:20 S-14: **Jun Koseki** (Osaka University, Japan)

Trans-omics analysis shows novel functional change in the ornithine metabolic pathway between cancer stem cells and non-cancer stem cells

14:20-14:55 S-15: **Marie Evangelista** (Genentech, USA)

Lessons from targeting metabolic dependencies in PDAC

14:55-15:00 Closing Remarks: **Hiroyuki Sasaki** (Kyushu University, Japan)

Session3: Short-Talk Session for Young Scientists Chair: **Tohru Ishitani**

Wednesday, November, 2 2016

14:45-16:45 Short talks of 12 minutes each

Y-01: **Shinjiro Hino** (Kumamoto University, Japan)

Regulation of cellular metabolism by histone demethylase LSD1

Y-02: **Kou Motani** (Tokushima University, Japan)

Identification of STING-dependent secreted proteins using quantitative proteomic analysis

Y-03: **Kenji Shimazu** (Tokushima University, Japan)

Characterization of target genes for inhibitory co-receptor PD-1 by CAGE

Y-04: **Yuki Kawasaki** (Tokyo Medical and Dental University, Japan)

Development of the novel method "EnIGMA" for simultaneous identification of methylcytosine and hydroxymethylcytosine

Y-05: **Yuki Akieda** (Kyushu University, Japan)

Apoptosis-mediated elimination of "Wnt/β-catenin signaling noise" supports precise embryonic patterning

Y-06: **Yuta Katayama** (Kyushu University, Japan)

CHD8 haploinsufficiency results in autistic-like phenotypes in mice

Y-07: **Ryusuke Sawada** (Kyushu University, Japan)

Transomics-based drug repositioning for a wide range of diseases

Y-08: **Kai Inui** (Kyushu University, Japan)

Analysis of nonsense-mediated mRNA decay (NMD) using genomic and transcriptomic data

Y-09: **Yuuta Imoto** (Kyushu University, Japan)

Post-genomic analysis of supramolecular nanomachinery for membrane-bounded organelle division

Y-10: **Yuki Sohma** (Kyushu University, Japan)

Metabolomics on designed metabolic dynamics by synthetic genetic circuits